

## SEQUENCE LISTING

&lt;110&gt; AstaCarotene AB

&lt;120&gt; DNA construct and its use

&lt;130&gt; 29295-AstaCarotene

&lt;140&gt;

&lt;141&gt;

&lt;160&gt; 2

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 2543

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: napin promoter  
+ chloroplast localization signal + beta-carotene C-4 oxygenase  
coding sequence + termination sequence

&lt;220&gt;

&lt;221&gt; promoter

&lt;222&gt; (1) .. (1145)

&lt;220&gt;

&lt;221&gt; transit\_peptide

&lt;222&gt; (1179) .. (1347)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1179) .. (2217)

&lt;220&gt;

&lt;221&gt; terminator

&lt;222&gt; (2273) .. (2536)

&lt;400&gt; 1

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Met Ala Ser Ser Met  
1 5  
ctc tct tcc gct act atg gtt gcc tct ccg gct cag gcc act atg gtc 1242  
Leu Ser Ser Ala Thr Met Val Ala Ser Pro Ala Gln Ala Thr Met Val  
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gct cct ttc aac gga ctt aag tcc tcc gct gcc ttc cca gcc acc cgc 1290  
Ala Pro Phe Asn Gly Leu Lys Ser Ser Ala Ala Phe Pro Ala Thr Arg  
25 30 35  
aag gct aac aac gac att act tcc atc aca agc aac ggc gga cgc gtt 1338  
Lys Ala Asn Asn Asp Ile Thr Ser Ile Thr Ser Asn Gly Gly Arg Val  
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aac tgc atg tct aga atg cca tcc gag tcg tca gac gca gct cgt cct 1386  
Asn Cys Met Ser Arg Met Pro Ser Glu Ser Ser Asp Ala Ala Arg Pro  
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gcg cta aag cac gcc tac aaa cct cca gca tct gac gcc aag ggc atc 1434  
Ala Leu Lys His Ala Tyr Lys Pro Pro Ala Ser Asp Ala Lys Gly Ile  
70 75 80 85  
acg atg gcg ctg acc atc att ggc acc tgg acc gca gtg ttt tta cac 1482  
Thr Met Ala Leu Thr Ile Ile Gly Thr Trp Thr Ala Val Phe Leu His  
90 95 100  
gca ata ttt caa atc agg cta ccg aca tcc atg gac cag ctt cac tgg 1530  
Ala Ile Phe Gln Ile Arg Leu Pro Thr Ser Met Asp Gln Leu His Trp  
105 110 115  
ttg cct gtg tcc gaa gcc aca gcc cag ctt ttg ggc gga agc agc agc 1578  
Leu Pro Val Ser Glu Ala Thr Ala Gln Leu Leu Gly Gly Ser Ser Ser  
120 125 130  
cta ctg cac atc gct gca gtc ttc att gta ctt gag ttc ctg tac act 1626  
Leu Leu His Ile Ala Ala Val Phe Ile Val Leu Glu Phe Leu Tyr Thr  
135 140 145

ggt cta ttc atc acc aca cat gac gca atg cat ggc acc ata gct ttg 1674  
 Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly Thr Ile Ala Leu  
 150 155 160 165

agg cac agg cag ctc aat gat ctc ctt ggc aac atc tgc ata tca ctg 1722  
 Arg His Arg Gln Leu Asn Asp Leu Leu Gly Asn Ile Cys Ile Ser Leu  
 170 175 180

tac gcc tgg ttt gac tac agc atg ctg cat cgc aag cac tgg gag cac 1770  
 Tyr Ala Trp Phe Asp Tyr Ser Met Leu His Arg Lys His Trp Glu His  
 185 190 195

cac aac cat act ggc gaa gtg ggg aaa gac cct gac ttc cac aag gga 1818  
 His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp Phe His Lys Gly  
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aat ccc ggc ctt gtc ccc tgg ttc gcc agc ttc atg tcc agc tac atg 1866  
 Asn Pro Gly Leu Val Pro Trp Phe Ala Ser Phe Met Ser Ser Tyr Met  
 215 220 225

tcc ctg tgg cag ttt gcc cgg ctg gca tgg tgg gca gtg gtg atg caa 1914  
 Ser Leu Trp Gln Phe Ala Arg Leu Ala Trp Trp Ala Val Val Met Gln  
 230 235 240 245

atg ctg ggg gcg ccc atg gca aat ctc cta gtc ttc atg gct gca gcc 1962  
 Met Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe Met Ala Ala Ala  
 250 255 260

cca atc ttg tca gca ttc cgc ctc ttc tac ttc ggc act tac ctg cca 2010  
 Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Leu Pro  
 265 270 275

cac aag cct gag cca ggc cct gca gca ggc tct cag gtg atg gcc tgg 2058  
 His Lys Pro Glu Pro Gly Pro Ala Ala Gly Ser Gln Val Met Ala Trp  
 280 285 290

ttc agg gcc aag aca agt gag gca tct gat gtg atg agt ttc ctg aca 2106  
 Phe Arg Ala Lys Thr Ser Glu Ala Ser Asp Val Met Ser Phe Leu Thr  
 295 300 305

tgc tac cac ttt gac ctg cac tgg gag cac cac aga tgg ccc ttt gcc 2154  
 Cys Tyr His Phe Asp Leu His Trp Glu His His Arg Trp Pro Phe Ala  
 310 315 320 325

ccc tgg tgg cag ctg ccc cac tgc cgc cgc ctg tcc ggg cgt ggc ctg 2202  
 Pro Trp Trp Gln Leu Pro His Cys Arg Arg Leu Ser Gly Arg Gly Leu  
 330 335 340

gtg cct gcc ttg gca tgacctgggc cctccgctgg tgaccagcg tctgcacaag 2257  
 Val Pro Ala Leu Ala  
 345

agtgtcatgg agctcgaatt tccccgatcg ttcaaacatt tggcaataaa gtttcttaag 2317

attgaatcct gttgccggtc ttgcgatgat tatcatataa tttctgttga attacgttaa 2377

gcatgtaata attaacatgt aatgcatgac gttatttatg agatggggtt ttatgattag 2437

agtccccgcaa ttatacathtt aatacgcgat agaaaacaaa atatagcgcg caaactagga 2497

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<210> 2  
 <211> 346  
 <212> PRT  
 <213> Artificial Sequence  
 <223> Description of Artificial Sequence: deduced fusion protein of  
 transit peptide + peptide with beta-carotene C-4 oxygenase activity

<400> 2

Met Ala Ser Ser Met Leu Ser Ser Ala Thr Met Val Ala Ser Pro Ala

1 5 10 15

Gln Ala Thr Met Val Ala Pro Phe Asn Gly Leu Lys Ser Ser Ala Ala  
 20 25 30

Phe Pro Ala Thr Arg Lys Ala Asn Asn Asp Ile Thr Ser Ile Thr Ser  
 35 40 45

Asn Gly Gly Arg Val Asn Cys Met Ser Arg Met Pro Ser Glu Ser Ser  
 50 55 60

Asp Ala Ala Arg Pro Ala Leu Lys His Ala Tyr Lys Pro Pro Ala Ser  
 65 70 75 80

Asp Ala Lys Gly Ile Thr Met Ala Leu Thr Ile Ile Gly Thr Trp Thr  
 85 90 95

Ala Val Phe Leu His Ala Ile Phe Gln Ile Arg Leu Pro Thr Ser Met  
 100 105 110

Asp Gln Leu His Trp Leu Pro Val Ser Glu Ala Thr Ala Gln Leu Leu  
 115 120 125

Gly Gly Ser Ser Ser Leu Leu His Ile Ala Ala Val Phe Ile Val Leu  
 130 135 140

Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His  
 145 150 155 160

Gly Thr Ile Ala Leu Arg His Arg Gln Leu Asn Asp Leu Leu Gly Asn  
 165 170 175

Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Ser Met Leu His Arg  
 180 185 190

Lys His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro  
 195 200 205

Asp Phe His Lys Gly Asn Pro Gly Leu Val Pro Trp Phe Ala Ser Phe  
 210 215 220

Met Ser Ser Tyr Met Ser Leu Trp Gln Phe Ala Arg Leu Ala Trp Trp  
 225 230 235 240

Ala Val Val Met Gln Met Leu Gly Ala Pro Met Ala Asn Leu Leu Val  
 245 250 255

Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe  
260 265 270

Gly Thr Tyr Leu Pro His Lys Pro Glu Pro Gly Pro Ala Ala Gly Ser  
275 280 285

Gln Val Met Ala Trp Phe Arg Ala Lys Thr Ser Glu Ala Ser Asp Val  
290 295 300

Met Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His His  
305 310 315 320

Arg Trp Pro Phe Ala Pro Trp Trp Gln Leu Pro His Cys Arg Arg Leu  
325 330 335

Ser Gly Arg Gly Leu Val Pro Ala Leu Ala  
340 345